

## SEQUENCE LISTING

&lt;110&gt; Consiglio Nazionale delle Ricerche

5 &lt;120&gt; Fusion proteins

&lt;130&gt; BW352R

&lt;160&gt; 7

&lt;170&gt; PatentIn version 3.2

10 &lt;210&gt; 1

&lt;211&gt; 732

&lt;212&gt; DNA

&lt;213&gt; Parietaria judaica

&lt;222&gt; (1)..(729)

15

&lt;220&gt;

&lt;221&gt; misc\_feature

<222> (10)..(12); (40)..(42); (85)..(90); (148)..(150); (154)..(156);  
(271)..(273); (322)..(324); (352)..(354); (397)..(402); (460)..(462);  
20 (466)..(468); (535)..(537); (583)..(585)

&lt;223&gt; n is a, c, g, or t

&lt;400&gt; 1

25 gag gag gct nnn ggg aaa gtg gtg cag gat ata atg ccg nnn ctg cat 48  
Glu Glu Ala Xaa Gly Lys Val Val Gln Asp Ile Met Pro Xaa Leu His  
1 5 10 1530 ttc gtg aag ggg gag gag aag gag ccg tcg aag gag nnn nnn agc ggc 96  
Phe Val Lys Gly Glu Glu Lys Glu Pro Ser Lys Glu Xaa Xaa Ser Gly  
20 25 3035 acg aag aag ctg agc gag gag gtg aag acg acg gag cag aag agg gag 144  
Thr Lys Lys Leu Ser Glu Glu Val Lys Thr Thr Glu Gln Lys Arg Glu  
35 40 45gcc nnn aag nnn ata gtg cgc gcc acg aag ggc atc tcc ggt atc aaa 192  
Ala Xaa Lys Xaa Ile Val Arg Ala Thr Lys Gly Ile Ser Gly Ile Lys  
50 55 6040 aat gaa ctt gtc gcc gag gtc ccc aag aag nnn gat att aag acc act 240  
Asn Glu Leu Val Ala Glu Val Pro Lys Lys Xaa Asp Ile Lys Thr Thr  
65 70 75 8045 ctc ccg ccc atc acc gcc gac ttc gac tgc nnn aag atc caa agt act 288  
Leu Pro Pro Ile Thr Ala Asp Phe Asp Cys Xaa Lys Ile Gln Ser Thr  
85 90 95att ttc aga ggt tac tat gga ttc caa gaa acc nnn ggg act atg gtg 336  
Ile Phe Arg Gly Tyr Tyr Gly Phe Gln Glu Thr Xaa Gly Thr Met Val  
100 105 110

50

aga gcg ctg atg ccg nnn ctg ccg ttc gtg cag ggg aaa gag aaa gag 384  
 Arg Ala Leu Met Pro Xaa Leu Pro Phe Val Gln Gly Lys Glu Lys Glu  
 115 120 125

5 ccg tca aag ggg nnn nnn agc ggc gcc aaa aga ttg gac ggg gag acg 432  
 Pro Ser Lys Gly Xaa Xaa Ser Gly Ala Lys Arg Leu Asp Gly Glu Thr  
 130 135 140

10 aag acg ggg ccg cag agg gtg cac gct nnn gag nnn atc cag acc gcc 480  
 Lys Thr Gly Pro Gln Arg Val His Ala Xaa Glu Xaa Ile Gln Thr Ala  
 145 150 155 160

15 atg aag act tat tcc gac atc gac ggg aaa ctc gtc agc gag gtc ccc 528  
 Met Lys Thr Tyr Ser Asp Ile Asp Gly Lys Leu Val Ser Glu Val Pro  
 165 170 175

aag cac nnn ggc atc gtt gac agc aag ctc ccg ccc att gac gtc aac 576  
 Lys His Xaa Gly Ile Val Asp Ser Lys Leu Pro Pro Ile Asp Val Asn  
 180 185 190

20 atg gac nnn aag aca gtt gga gtg gtt cct ccg caa ccc caa ctt cca 624  
 Met Asp Xaa Lys Thr Val Gly Val Val Pro Arg Gln Pro Gln Leu Pro  
 195 200 205

25 gtc tct ctc cgt cat ggt ccc gtc acg ggc cca agt gat ccc gcc cac 672  
 Val Ser Leu Arg His Gly Pro Val Thr Gly Pro Ser Asp Pro Ala His  
 210 215 220

30 aaa gca cgg ttg gag aga ccc cag att aga gtt ccg ccc ccc gca ccg 720  
 Lys Ala Arg Leu Glu Arg Pro Gln Ile Arg Val Pro Pro Pro Ala Pro  
 225 230 235 240

gaa aaa gcc taa 732  
 Glu Lys Ala

35

40 <210> 2  
 <211> 243  
 <212> PRT  
 <213> Parietaria judaica

45 <220>  
 <221> misc\_feature  
 <222> (4)..(4)  
 <223> The 'Xaa' at location 4, 14, 29, 30, 50, 52, 75, 91, 108, 118, 133,  
 154, 156, 179, 195 stands for Asn, Ser, Thr, Ile, Met, Gly, Ala, Val, Gln or  
 Leu.

50 <400> 2

Glu Glu Ala Xaa Gly Lys Val Val Gln Asp Ile Met Pro Xaa Leu His  
1 5 10 15

5 Phe Val Lys Gly Glu Glu Lys Glu Pro Ser Lys Glu Xaa Xaa Ser Gly  
20 25 30

Thr Lys Lys Leu Ser Glu Glu Val Lys Thr Thr Glu Gln Lys Arg Glu  
35 40 45

10 Ala Xaa Lys Xaa Ile Val Arg Ala Thr Lys Gly Ile Ser Gly Ile Lys  
50 55 60

Asn Glu Leu Val Ala Glu Val Pro Lys Lys Xaa Asp Ile Lys Thr Thr  
15 65 70 75 80

Leu Pro Pro Ile Thr Ala Asp Phe Asp Cys Xaa Lys Ile Gln Ser Thr  
85 90 95

20 Ile Phe Arg Gly Tyr Tyr Gly Phe Gln Glu Thr Xaa Gly Thr Met Val  
100 105 110

Arg Ala Leu Met Pro Xaa Leu Pro Phe Val Gln Gly Lys Glu Lys Glu  
115 120 125

25 Pro Ser Lys Gly Xaa Xaa Ser Gly Ala Lys Arg Leu Asp Gly Glu Thr  
130 135 140

Lys Thr Gly Pro Gln Arg Val His Ala Xaa Glu Xaa Ile Gln Thr Ala  
30 145 150 155 160

Met Lys Thr Tyr Ser Asp Ile Asp Gly Lys Leu Val Ser Glu Val Pro  
165 170 175

35 Lys His Xaa Gly Ile Val Asp Ser Lys Leu Pro Pro Ile Asp Val Asn  
180 185 190

Met Asp Xaa Lys Thr Val Gly Val Val Pro Arg Gln Pro Gln Leu Pro  
40 195 200 205

Val Ser Leu Arg His Gly Pro Val Thr Gly Pro Ser Asp Pro Ala His  
210 215 220

45 Lys Ala Arg Leu Glu Arg Pro Gln Ile Arg Val Pro Pro Pro Ala Pro  
225 230 235 240

Glu Lys Ala  
50

<210> 3  
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 Glu Glu Ala Ser Gly Lys Val Val Gln Asp Ile Met Pro Cys Leu His  
 1 5 10 15  
  
 15 ttc gtg aag ggg gag gag aag gag ccg tgc aag gag agc agc agc ggc 96  
 Phe Val Lys Gly Glu Glu Lys Glu Pro Ser Lys Glu Ser Ser Ser Gly  
 20 25 30  
  
 20 acg aag aag ctg agc gag gag gtg aag acg acg gag cag aag agg gag 144  
 Thr Lys Lys Leu Ser Glu Glu Val Lys Thr Thr Glu Gln Lys Arg Glu  
 35 40 45  
  
 25 gcc tgc aag tgc ata gtg cgc gcc acg aag ggc atc tcc ggt atc aaa 192  
 Ala Cys Lys Cys Ile Val Arg Ala Thr Lys Gly Ile Ser Gly Ile Lys  
 50 55 60  
  
 30 aat gaa ctt gtc gcc gag gtc ccc aag aag tgc gat att aag acc act 240  
 Asn Glu Leu Val Ala Glu Val Pro Lys Lys Cys Asp Ile Lys Thr Thr  
 65 70 75 80  
  
 35 ctc ccg ccc atc acc gcc gac ttc gac tgc tcc aag atc caa agt act 288  
 Leu Pro Pro Ile Thr Ala Asp Phe Asp Cys Ser Lys Ile Gln Ser Thr  
 85 90 95  
  
 40 att ttc aga ggt tac tat gga ttc caa gaa acc agc ggg act atg gtg 336  
 Ile Phe Arg Gly Tyr Tyr Gly Phe Gln Glu Thr Ser Gly Thr Met Val  
 100 105 110  
  
 45 aga gcg ctg atg ccg tgc ctg ccg ttc gtg cag ggg aaa gag aaa gag 384  
 Arg Ala Leu Met Pro Cys Leu Pro Phe Val Gln Gly Lys Glu Lys Glu  
 115 120 125  
  
 50 ccg tca aag ggg agc agc agc ggc gcc aaa aga ttg gac ggg gag acg 432  
 Pro Ser Lys Gly Ser Ser Ser Gly Ala Lys Arg Leu Asp Gly Glu Thr  
 130 135 140  
  
 45 aag acg ggg ccg cag agg gtg cac gct tgt gag tgc atc cag acc gcc 480  
 Lys Thr Gly Pro Gln Arg Val His Ala Cys Glu Cys Ile Gln Thr Ala  
 145 150 155 160  
  
 50 atg aag act tat tcc gac atc gac ggg aaa ctc gtc agc gag gtc ccc 528  
 Met Lys Thr Tyr Ser Asp Ile Asp Gly Lys Leu Val Ser Glu Val Pro  
 165 170 175

aag cac tgc ggc atc gtt gac agc aag ctc ccg ccc att gac gtc aac 576  
 Lys His Cys Gly Ile Val Asp Ser Lys Leu Pro Pro Ile Asp Val Asn  
 180 185 190

5 atg gac tgc aag aca gtt gga gtg gtt cct cgg caa ccc caa ctt cca 624  
 Met Asp Cys Lys Thr Val Gly Val Val Pro Arg Gln Pro Gln Leu Pro  
 195 200 205

10 gtc tct ctc cgt cat ggt ccc gtc acg ggc cca agt gat ccc gcc cac 672  
 Val Ser Leu Arg His Gly Pro Val Thr Gly Pro Ser Asp Pro Ala His  
 210 215 220

15 aaa gca cgg ttg gag aga ccc cag att aga gtt ccg ccc ccc gca ccg 720  
 Lys Ala Arg Leu Glu Arg Pro Gln Ile Arg Val Pro Pro Pro Ala Pro  
 225 230 235 240

gaa aaa gcc taa 732  
 Glu Lys Ala

20

<210> 4  
 <211> 243  
 <212> PRT  
 25 <213> Parietaria judaica

<400> 4

30 Glu Glu Ala Ser Gly Lys Val Val Gln Asp Ile Met Pro Cys Leu His  
 1 5 10 15

Phe Val Lys Gly Glu Glu Lys Glu Pro Ser Lys Glu Ser Ser Ser Gly  
 20 25 30

35 Thr Lys Lys Leu Ser Glu Glu Val Lys Thr Thr Glu Gln Lys Arg Glu  
 35 40 45

Ala Cys Lys Cys Ile Val Arg Ala Thr Lys Gly Ile Ser Gly Ile Lys  
 50 55 60

40 Asn Glu Leu Val Ala Glu Val Pro Lys Lys Cys Asp Ile Lys Thr Thr  
 65 70 75 80

Leu Pro Pro Ile Thr Ala Asp Phe Asp Cys Ser Lys Ile Gln Ser Thr  
 45 85 90 95

Ile Phe Arg Gly Tyr Tyr Gly-Phe Gln Glu Thr Ser Gly Thr Met Val  
 100 105 110

50 Arg Ala Leu Met Pro Cys Leu Pro Phe Val Gln Gly Lys Glu Lys Glu  
 115 120 125

Pro Ser Lys Gly Ser Ser Ser Gly Ala Lys Arg Leu Asp Gly Glu Thr  
 130 135 140  
 Lys Thr Gly Pro Gln Arg Val His Ala Cys Glu Cys Ile Gln Thr Ala  
 5 145 150 155 160  
 Met Lys Thr Tyr Ser Asp Ile Asp Gly Lys Leu Val Ser Glu Val Pro  
 165 170 175  
 Lys His Cys Gly Ile Val Asp Ser Lys Leu Pro Pro Ile Asp Val Asn  
 10 180 185 190  
 Met Asp Cys Lys Thr Val Gly Val Val Pro Arg Gln Pro Gln Leu Pro  
 195 200 205  
 Val Ser Leu Arg His Gly Pro Val Thr Gly Pro Ser Asp Pro Ala His  
 15 210 215 220  
 Lys Ala Arg Leu Glu Arg Pro Gln Ile Arg Val Pro Pro Pro Ala Pro  
 20 225 230 235 240  
 Glu Lys Ala  
 25 <210> 5  
 <211> 18  
 <212> DNA  
 <213> Artificial  
 30 <220>  
 <223> forward primer for insertion of mutation in position 29 and 30  
 <400> 5  
 gagagcagca gcggcagc 18  
 35 <210> 6  
 <211> 30  
 <212> DNA  
 <213> Artificial  
 40 <220>  
 <223> forward primer for insertion of mutation in position 4  
 <400> 6  
 45 gtgggatccg aggaggctag cgggaaagtg 30  
 <210> 7  
 <211> 24  
 <212> DNA  
 50 <213> Artificial

&lt;220&gt;

&lt;223&gt; reverse parj2 primer

&lt;400&gt; 7

5 gggggatcca tagtaacctc tgaa

24